





US-09-417- 1716 agGagTCGAGaAGCGA gagcACTcgGcgGaggtgtgaaagagcTCTGCT  
+ + + + +  
US-09-417- 1530 CAGTTCGAG TCCTGA aagccTaaCTTCTGAGCCAA TCTGCTGA  
+ + + + +  
US-09-417- 1536 AccaactcaacttcctgtatgccaagcgagacCTTGatGCGAAAgaaagccaaagtTAgTGA  
+ + + + +  
consensus -ag--tGgagaACgcatgaty----ggg-AgtctGa-Gccaaag-ga-----tGtGtGa  
US-09-417- 1766  
US-09-417- 1576 TG acgaactCAAAAGcaagAA  
+ + + + +  
US-09-417- 1576 TC CCAAAAG ACA  
+ + + + +  
US-09-417- 1656 TctgaagatgatattatgaggaagttaagtgatataatttattattatctgaacatgatACGA  
+ + + + +  
US-09-417- 1656 tgtgaagatgatattatgaggaagttaagtgatataatttatt-----caaaag--caga  
+ + + + +  
consensus  
US-09-417- 1784 ctgtAAAGAGcTcagcggtctgagatgtgtgtgagtgatcagGtGGAAttcCAcTCA  
+ + + + +  
US-09-417- 1587 gccCAAAAGAGC agcGCcaactGaCGtAAAgagtgatTgt  
+ + + + +  
US-09-417- 1717 cagatgtAtgcatactgtgtgactgctgagggagagaataaccagAcTgctCtctccccaTgccaata  
+ + + + +  
consensus c-g-aaAgagC--g-g--ga-g-----a--a-C--g-cg-aa--t-ga--t-a  
US-09-417- 1845 atCAgaTgaTgcatactTgtgtgAGtgcgagtgagtggtggtccTgaaggagagcACAGCAG  
+ + + + +  
US-09-417- 1626 gAAgacTCTtaaaTAgTtTGtAGctattatccCatctTtATGcaactTtTtCGAGCTG  
+ + + + +  
US-09-417- 1778 aAAaacaacGcgagAgTcgggGaaGaaGaaAcataTgcAgagcaCTAtgtATTgactattaac  
+ + + + +  
consensus aAA-aa-tcga--a-tgttggg-aag--a-a-c-c--t--cAtg-g--tt--gcagcag  
US-09-417- 1906 agAtgagTgcttACTgtctTAGAGAGaGaaatGAAATcaGcaactATcAAATaaatcaaa  
+ + + + +  
US-09-417- 1687 cCAgATTTTAgACcAtatGAGAGA ctGGAAT taAAAGaaAT gTtTtct  
+ + + + +  
US-09-417- 1839 tTAAATTTTTCaAtctgggcatttA gaA ttTgggttgagACT caataa  
+ + + + +  
consensus --A-atTtTta-Acc--t-gagagAgg-aagaaat-----taa--AAaTaa--t-laa  
US-09-417- 1967 TTTCattaaaaaataaaaaaataTAAATAAATAAATAAATAAATAA  
+ + + + +  
US-09-417- 1738 TTTC CtTtTtctTAggAAATAAATAAATAAATAAATAAATAA  
+ + + + +  
US-09-417- 1890 atTC CccctTaaatTctTAAATAAATAAATAAATAAATAA  
+ + + + +  
consensus tTTCattaaaaac---ttaaata-tAAATAAATAAATAAATAAATAAATAAATAA  
US-09-417- 2028 aaaa  
US-09-417- 1775  
US-09-417- 1928 aactcgagactagttc  
consensus aa--cgaagactagttc

Alignment score = -1017.00  
Scoring matrix:

4  
5  
8

4	-	296	345
5	-		-396
8	-		

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GENALIGN - Multiple Sequence Alignment Program  
Release 5.4

Wed 21 Nov 101 12:09:59-PST

Solution Parameters:

Amino Alphabet = Identity  
Output line length = 80  
Compress = Off  
Histogram = Off  
Randomization = Off  
AMINO-Res-length = 2  
Deletion-weight = 5.00  
Length-factor = 0  
Matching-weight = 1.00  
NUCLEIC-Res-length = 4  
Spread-factor = 50

Clustered order of selected sequences:

4. US-09-417-251-8 (1-541)  
8. US-09-417-251-16 (1-551)  
5. US-09-417-251-10 (1-570)

Region Alignment: (listed in Clustered order)

US-09-417- 1 heepdaaagasaahlpdfigfeggaedED fgdffsdf  
US-09-417- 1 mriIvVL SLAT lllfssllfllcDDL tddEDdgfldepsaapbhghy  
US-09-417- 1 mgstlmspsfpyvllllllLARIaaagsmdeevvDdLgylldnsddipLndpddgwppegd  
consensus mgstlmsp-----vvl-----lAt--a-a-s-1-----ddl-----ded-----g-----

US-09-417- 38 ebsDA DrdeYkAPEVDEKDVVVLKegNfAdfVeKnfVWVEFYAPWCGHCOALA  
US-09-417- 48 hDDDAIfgdfeepeaYKQPEVDEKDVVLLKEKNfCDtYKSNFVWVEFYAPWCGHCOALA  
US-09-417- 62 yDDdDdlIfgdqgdqdlIghQPEIdethvVlaaaNfssFlaSShhVWVEFYAPWCGHCOALA  
consensus -DdDa-----d---yKqPEVDEKdVvVlKe-NfAdfV-snrfVWVEFYAPWCGHCOALA

US-09-417- 92 P EYAAATBELKGenVLAkVDATEENELsOKYdVQGFPTVYFFADGvHKsYpGQR  
US-09-417- 109 P EYAAATBELKGeVlLAkVDATEENELAQYdVQGFPTVhFEVdGjHKpYNGQR  
US-09-417- 123 pgiStrrrhLAgstnpPrnfaLAKVDATEEtdLAQYdVQGFPTlIfFIdGvPrigYNGAR  
consensus PgiStrreyaaAaTeIkgenV-LAKVDATEENELaQkYdVQGFPTV-FF-DGvNh-YngQR

US-09-417- 147 TKDAIVTWlKKRIGPgiVNIstVEDAErILtStKtVVLGyLNSLVGPEsNELAAASRLLED  
US-09-417- 164 TKDAIVTWlGKRIGPgiVNIstVEDAQrILtNEtKtVVLGfLNSLVGPESeLELAASRLLED  
US-09-417- 184 tKEaIVdWlNKRIgPeVqVNTsYdEaQsILtYgdkavLaFLdLtsGahSdELAAASRLLEDs  
consensus TKDAIVtWl-KKIGPgiYn-TsYedAqriLlT-etKvVLGfLNSLVGPes-ELAAASRLLEDd

US-09-417- 208 vNFYQTVdPeVAKLFHIEasAKRPALVLLKKEaEKLnRFdGeFSKaIaeFvFANKLPLVT  
US-09-417- 225 vNFYQTVdPeVAKLFHIDpdkRPALlVwKKEEKLnHfEdGfKekSeIadFvFSNKLPLVT  
consensus vNFYQTVdPeVAKLFHIDpdkRPALlVwKKEEKLnHfEdGfKekSeIadFvFSNKLPLVT

US-09-417- 245 INFYQTSbPDVAKLFHIDAaAKRPsvLLlKKEEKlLfYdGeFkaSaIngFvSANKLPLVT  
consensus vNFYQTVdPeVAKLFHIda-akRPALVLLKKEaEKLn-IDGeF-KSaIn-FvFANKLPLVT

US-09-417- 269 kFTRESAPllFEESIKKQlLlFAISNDSEKlPIFEESsKSPFGKLIFFvVEIdJNDVGKP  
US-09-417- 286 lFTRESAPsvFEERIKKQlLlFAtSNDSEKlPAfKEAKSPFGKLIFFvVEIdJNDVGKP  
US-09-417- 306 lITgELSPSlFgNPRIKQlLlFvaseStKlPIfKEAKSPFGKLIFFvVEIdJNDVGKP  
consensus -lFTRESAPslFenPIKKQlLlFA-sndSEKlPIfKEaKSPFGKLIFFvVE-DndVGKP

US-09-417- 330 vSFYFGISGNgPvLdYGTGnEdSKRPvLaKEVtIdnIKaFgenFLedKlKPFYKSdPvES  
US-09-417- 347 vSEYfGISGNaPvLdYGTGnDgKRPvLdGEvAdIKaFGddFLedKlKPFYKSdPvES  
US-09-417- 367 vAdYfGILtGqetVLAyTGnEdarkfLDGEvSleakIdFaegFLedKlLFPYKSdPvES  
consensus vseYfGISGn-p-VlGYTGnEd-KRPvLdGEvLd-IkaFge-FLedKlKPFYKSdPvES

US-09-417- 391 NDGDVkvVvGdNEdNlVLDSEKDVLEIYApmWCGHCOALEPtyNKLAKHLRgIdSLVIAM  
US-09-417- 408 NDGDVkvIvGnNDeIVLDSEKDVLEIYApmWCGHCOALEPIdKLAKHLRtESLVIAM  
US-09-417- 428 NDGDVkvIvGKNlDlIVfEdCKDVLEIYApmWCGHCOsLEPtlNKLAKHLRsvdSLVIAM  
consensus NDGDVkvIvG-NfD-IVIdESKDVLEIYApmWCGHCOALEPtyNKLAKHLR-IdSLVIAM

US-09-417- 452 DGTtNEHPRAKSDGfPTlLFFPaGnKSPdITVDTDRtVAlYKfIKKNaStPFKlQKpvs  
US-09-417- 469 DGTtNEHPRAKSDGfPTlLFFPaGnKSPdITVDTDRtVAlYKfIKKNaStPFKlQKp  
US-09-417- 489 DGTtNEHPRAKSDGfPTlLFFPaGnKSPdITVDTDRtVAlYKfIKKNaStPFKlQKp  
consensus DGTtNEHPRAKSDGfPTlLFFPaGnKSPdITVDTDRtVAlYKfIKKNaStPFKlQKpvs

US-09-417- 513 spKvSsEaKSGPaKESpKStLdVKDEL  
US-09-417- 528 tStsdakYSSPAKES qSS DVKDEL  
US-09-417- 545 krgEstESCrabgYvKSSgtnSKDEL  
consensus sp---s-----ssdakEs-KSS-LdVKDEL

Alignment score = 411.00  
Scoring matrix:

4	94	289
5		213
8		

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